

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Zabeau, Marc
Vos, Pieter
Simons, Guus
- (ii) TITLE OF INVENTION: RESISTANCE AGAINST WILT INDUCING FUNGI
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SPENCER & FRANK
 - (B) STREET: 1100 New York Avenue, N.W., Suite 300 East
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/EP96/03480
 - (B) FILING DATE: 06-AUG-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP 95401849.5
 - (B) FILING DATE: 07-AUG-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gollin, Michael A.
 - (B) REGISTRATION NUMBER: 31,957
 - (C) REFERENCE/DOCKET NUMBER: GUPLA 0008
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-414-4000
 - (B) TELEFAX: 202-414-4040

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACTGCGTAC CAATTCNNN

19

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATGAGTCCT GAGTAANNN

19

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCGTAGACT GCGTACC

17

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTGGTACG CAGTCTAC

18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGATGAGT CCTGAG

16

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACTCAGGAC TCAT

14

- (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACTGCGTAC CAATTC

16

- (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATGAGTCCT GAGTAA

16

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTGCGTAC CAATTCAGA

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATGAGTCCT GAGTAATCT

19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1798..5595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAAAAAGCAG	CTTTAAAAAA	AGTACTTTKG	AAAGGKGCTG	AAACTTATTT	TTTGAAATAA	60
GCAGTTATGT	GTTTGGAAWA	AAAGTGCTGA	AGTTGCTATG	TCAAACATGA	AAAGGGRAAA	120
AATGGAAGAA	AGAGWTGTTA	GGGTTATGTC	GTAATTTGGA	GATTGTATAA	AAATATTAAG	180
GGCAAAAAAA	ATAAAAATGT	GTCAACTTAA	AACAGCTTAT	AAGCTAAAAG	TTAAAAGCTG	240
GGGTAGAGGT	GTTTTTTTTT	TTTTTAGCTT	ATAAGTTGTT	TTAAGTTGAC	CACATTTTTA	300
TTTTTKTTGC	CCTTAATATT	TTTATACAAT	CTCAAATAA	CGACATAACC	CTAACATCTT	360
TTTCTCCCAT	TTTTTCCTTT	TCACGTTTGA	CATAGCAACT	TCAGCACTTT	TATCCAAACA	420
CATAACTGCT	TATTTTAAAA	ATAAGTTTCA	GCACTTTCAA	AAGTACTTTT	TTAAAGCTGC	480
TTTTATTAAG	CCCATCCAAA	CGGGCCCTAA	AATTGCTAAT	GTTTGCTCTT	TCTATTCTCA	540
AACTCCGTAA	TATTTAAGAA	AATTTGCTAA	TGATAGGTCA	CTTTTAACAC	TAAATAATTA	600
TAAATTGGGT	AGAAATTTAT	TTATCATTTT	AAGCTTTTTT	AATTTTGAGT	CTTCTCCCTA	660
ATTAAGACCC	TTCCCCTCTT	GCTTCAATTA	TTTAACTGAA	TAGTCTTTGT	CTTATTGTTG	720
GGTGAAAGTC	TGTCTTCTTG	TTAGGTACTA	AGTCCTACAA	TAATATCAAT	AATTTGCTAT	780
GGAGAAAAAA	ATATTATAGG	AGAAAAATAA	TTAATTTTAA	TTCATGAATA	TGTCTTAATA	840
TGCAACTCAT	TTTGCTTATA	TATATCAAAT	TAAACTCTGT	TCCTTTAACT	TTTTCCTATG	900
AAGATACATT	TTAATTTATT	TGATGAGGTT	AGTTTTGAAA	TTTATATTAT	AATAATGAAA	960
TGATATAACT	TAAAAGAAGT	TGTTTGATAT	CTTATCAGAA	TCATGCAGGT	ACTCATAATA	1020
TAAGAAATAA	TTATGATGAA	ATTTATATAT	GTTTTATGCA	GAGATTTATT	ACGCATTGTT	1080
TACTTGGGTT	ATGTATTACT	TATTTCATCT	TTTATCAGAA	TGTAAAATTA	TCATTCAATA	1140
AGAAATCCAA	TTCTGTAAAA	TTCAAAATAC	AAACAATAAC	ATTTTCAAGA	CCGATTTTTT	1200
GCCCAAGAAT	ATACAGTAAA	CATATTTATG	ATATGGTAGG	TCTCTTTAGT	AATTGACCAA	1260
CAAGGATTGT	GGTGGAGTGG	GAAATACTCT	TTAATACTTC	ACCAAGAGGT	CTCCAATTTG	1320
AGCCCCTGAA	TACGAAATCG	TCTTTGTTAG	TATATACCCT	AACCTAATAC	AAAAATTAGT	1380
ATATTAGCCT	TNACAGCTAA	AATCTTTGTG	ACCTGTAAGT	CACGCGAGGA	CAAATTTACC	1440
GTAACACCAA	CTTATTCATG	ATATAATTGT	CCCTTTTAGC	ACGGTAATAA	TGAGGTGGGT	1500
AGAAATTTAT	TACTTGAGGG	CCCTTTCTAC	ACCCACCCTT	ATTCTCTTGC	TTCAATTATT	1560
GAATTGAAGA	AGTAATGAAA	AAACAGACTC	CATTGGATAA	AGGACAGTTT	GCAAACACAG	1620
CTGTAACAAT	TTAGAGCACT	AGCAAAATAG	AGAGAGTTTT	GAGAGAAATT	TTTGTTTGCA	1680
AATTACTCTT	AACCTTCAGC	AGGTAAAATA	AAGTTCTTAA	CTGAGACTAT	TTGAAGATAT	1740
ATTTTGTTAA	AGAATCATTT	TGTGTGTTTC	CTTGTTTTGC	TTTTGCAGAT	TTGAGAA	1797

ATG Met 1	GAG Glu	ATT Ile	GGC Gly	TTA Leu 5	GCA Ala	GTT Val	GGT Gly	GGT Gly	GCA Ala 10	TTT Phe	CTC Leu	TCC Ser	TCA Ser	GCT Ala 15	TTG Leu	1845
AAT Asn	GTT Val	CTG Leu	TTT Phe 20	GAT Asp	AGG Arg	CTT Leu	GCT Ala	CCT Pro 25	AAC Asn	GGT Gly	GAT Asp	CTG Leu	CTC Leu 30	AAC Asn	ATG Met	1893
TTT Phe	CGG Arg	AAG Lys 35	CAT His	AAG Lys	GAT Asp	CAT His	GTT Val 40	AAG Lys	CTC Leu	TTA Leu	AAG Lys	AAG Lys 45	CTG Leu	AAA Lys	ATG Met	1941
ACT Thr 50	TTG Leu	CGT Arg	GGT Gly	ATT Ile	CAG Gln	ATT Ile 55	GTG Val	CTA Leu	AGT Ser	GAT Asp	GCA Ala 60	GAG Glu	AAT Asn	AAG Lys	CAA Gln	1989
GCA Ala 65	TCA Ser	AAT Asn	CCA Pro	TCT Ser	GTG Val 70	AGA Arg	GAC Asp	TGG Trp	CTT Leu	AAT Asn 75	GAG Glu	CTT Leu	CGA Arg	GAT Asp	GCT Ala 80	2037
GTC Val	GAC Asp	TCT Ser	GCT Ala	GAA Glu 85	AAT Asn	TTA Leu	ATA Ile	GAA Glu	GAA Glu 90	GTC Val	AAT Asn	TAT Tyr	GAA Glu	GCT Ala 95	TTG Leu	2085
AGG Arg	CTT Leu	AAG Lys 100	GTG Val	GAA Glu	GGT Gly	CAG Gln	CAT His	CAG Gln 105	AAT Asn	TTT Phe	TCA Ser	GAA Glu 110	ACA Thr	AGC Ser	AAC Asn	2133
CAG Gln	CAA Gln 115	GTA Val	AGT Ser	GAT Asp	GAT Asp	TTT Phe 120	TTC Phe	CTT Leu	AAC Asn	ATA Ile	AAG Lys	GAC Asp 125	AAG Lys	CTG Leu	GAA Glu	2181
GAC Asp 130	ACT Thr	ATT Ile	GAA Glu	ACA Thr	TTA Leu	AAG Lys 135	GAT Asp	TTG Leu	CAA Gln	GAG Glu	CAA Gln 140	ATT Ile	GGT Gly	CTC Leu	CTT Leu	2229
GGC Gly 145	TTA Leu	AAG Lys	GAG Glu	TAT Tyr	TTT Phe 150	GAT Asp	TCC Ser	ACG Thr	AAA Lys	CTA Leu 155	GAA Glu	ACT Thr	AGA Arg	AGA Arg	CCT Pro 160	2277
TCA Ser	ACT Thr	TCT Ser	GTG Val	GAT Asp 165	GAT Asp	GAA Glu	TCT Ser	GAT Asp	ATC Ile 170	TTT Phe	GGT Gly	AGG Arg	CAG Gln	AGC Ser	GAA Glu 175	2325
ATA Ile	GAG Glu	GAT Asp 180	TTG Leu	ATT Ile	GAC Asp	CGT Arg	CTA Leu	TTG Leu 185	TCT Ser	GAA Glu	GGT Gly	GCA Ala	AGT Ser 190	GGG Gly	AAA Lys	2373
AAG Lys	CTG Leu	ACA Thr 195	GTA Val	GTT Val	CCT Pro	ATC Ile 200	GTT Val	GGA Gly	ATG Met	GGC Gly	GGC Gly	CAG Gln 205	GGC Gly	AAG Lys	ACA Thr	2421
ACA Thr 210	CTT Leu	GCT Ala	AAA Lys	GCC Ala	GTA Val	TAC Tyr 215	AAT Asn	GAT Asp	GAG Glu	AGG Arg	GTG Val 220	AAG Lys	AAT Asn	CAT His	TTT Phe	2469
GAT Asp 225	TTG Leu	AAA Lys	GCG Ala	TGG Trp	TAT Tyr 230	TGC Cys	GTT Val	TCT Ser	GAA Glu	GGA Gly 235	TTT Phe	GAT Asp	GCT Ala	TTG Leu	AGA Arg 240	2517

ATA	ACA	AAA	GAA	TTA	CTC	CAA	GAA	ATT	GGC	AAA	TTT	GAC	TCG	AAG	GAT	2565
Ile	Thr	Lys	Glu	Leu	Leu	Gln	Glu	Ile	Gly	Lys	Phe	Asp	Ser	Lys	Asp	
				245					250					255		
GTC	CAC	AAC	AAT	CTT	AAC	CAG	CTT	CAA	GTC	AAA	TTG	AAG	GAA	AGT	TTG	2613
Val	His	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Val	Lys	Leu	Lys	Glu	Ser	Leu	
			260					265					270			
AAG	GGA	AAG	AAG	TTC	CTT	ATT	GTT	TTG	GAT	GAT	GTG	TGG	AAT	GAA	AAT	2661
Lys	Gly	Lys	Lys	Phe	Leu	Ile	Val	Leu	Asp	Asp	Val	Trp	Asn	Glu	Asn	
		275					280					285				
TAC	AAC	GAG	TGG	AAT	GAC	TTG	AGA	AAT	ATT	TTT	GCA	CAA	GGA	GAT	ATA	2709
Tyr	Asn	Glu	Trp	Asn	Asp	Leu	Arg	Asn	Ile	Phe	Ala	Gln	Gly	Asp	Ile	
	290					295					300					
GGA	AGT	AAG	ATC	ATT	GTG	ACG	ACA	CGC	AAA	GAC	AGT	GTT	GCC	TTG	ATG	2757
Gly	Ser	Lys	Ile	Ile	Val	Thr	Thr	Arg	Lys	Asp	Ser	Val	Ala	Leu	Met	
305					310					315					320	
ATG	GGA	AAT	GAG	CAA	ATT	CGC	ATG	GGC	AAT	TTG	TCT	ACC	GAA	GCC	TCT	2805
Met	Gly	Asn	Glu	Gln	Ile	Arg	Met	Gly	Asn	Leu	Ser	Thr	Glu	Ala	Ser	
				325					330					335		
TGG	TCT	TTA	TTT	CAA	AGA	CAT	GCA	TTT	GAA	AAC	ATG	GAT	CCT	ATG	GGA	2853
Trp	Ser	Leu	Phe	Gln	Arg	His	Ala	Phe	Glu	Asn	Met	Asp	Pro	Met	Gly	
			340					345					350			
CAT	CCG	GAA	CTT	GAA	GAG	GTC	GGA	AGA	CAA	ATT	GCA	GCC	AAG	TGC	AAA	2901
His	Pro	Glu	Leu	Glu	Glu	Val	Gly	Arg	Gln	Ile	Ala	Ala	Lys	Cys	Lys	
		355					360					365				
GGA	CTG	CCC	TTA	GCT	CTG	AAG	ACG	CTC	GCT	GGC	ATG	TTA	CGC	TCC	AAA	2949
Gly	Leu	Pro	Leu	Ala	Leu	Lys	Thr	Leu	Ala	Gly	Met	Leu	Arg	Ser	Lys	
	370					375					380					
TCA	GAG	GTT	GAA	GAG	TGG	AAA	CGT	ATT	TTG	AGA	AGT	GAA	ATA	TGG	GAG	2997
Ser	Glu	Val	Glu	Glu	Trp	Lys	Arg	Ile	Leu	Arg	Ser	Glu	Ile	Trp	Glu	
385					390					395					400	
CTG	CCA	CAC	AAT	GAC	ATA	TTA	CCA	GCG	TTG	ATG	TTG	AGC	TAC	AAT	GAT	3045
Leu	Pro	His	Asn	Asp	Ile	Leu	Pro	Ala	Leu	Met	Leu	Ser	Tyr	Asn	Asp	
				405					410					415		
CTT	CCC	GCA	CAT	TTA	AAG	CGA	TGC	TTT	TCT	TTT	TGT	GCA	ATA	TTT	CCT	3093
Leu	Pro	Ala	His	Leu	Lys	Arg	Cys	Phe	Ser	Phe	Cys	Ala	Ile	Phe	Pro	
			420					425					430			
AAA	GAT	TAT	CCA	TTT	AGG	AAA	GAA	CAA	GTT	ATT	CAT	CTA	TGG	ATT	GCC	3141
Lys	Asp	Tyr	Pro	Phe	Arg	Lys	Glu	Gln	Val	Ile	His	Leu	Trp	Ile	Ala	
		435					440					445				
AAT	GGT	CTC	GTA	CCA	GTG	AAA	GAT	GAA	ATA	AAT	CAA	GAT	TTA	GGC	AAC	3189
Asn	Gly	Leu	Val	Pro	Val	Lys	Asp	Glu	Ile	Asn	Gln	Asp	Leu	Gly	Asn	
	450					455					460					
CAA	TAC	TTT	CTA	GAG	TTG	AGA	TCA	AGA	TCA	TTA	TTT	GAA	AAG	GTC	CCA	3237
Gln	Tyr	Phe	Leu	Glu	Leu	Arg	Ser	Arg	Ser	Leu	Phe	Glu	Lys	Val	Pro	
465					470					475					480	

AAT	CCT	TCT	AAA	AGG	AAC	ATA	GAG	GAA	TTA	TTC	CTT	ATG	CAT	GAC	CTT	3285
Asn	Pro	Ser	Lys	Arg	Asn	Ile	Glu	Glu	Leu	Phe	Leu	Met	His	Asp	Leu	
				485					490					495		
GTC	AAT	GAT	TTA	GCC	CAA	CTT	GCA	TCT	TCA	AAA	CTT	TGT	ATC	AGG	TTA	3333
Val	Asn	Asp	Leu	Ala	Gln	Leu	Ala	Ser	Ser	Lys	Leu	Cys	Ile	Arg	Leu	
			500					505					510			
GAA	GAG	AGC	CAA	GGA	TCT	CAT	ATG	TTG	GAA	CAA	TGT	CGG	CAC	TTA	TCT	3381
Glu	Glu	Ser	Gln	Gly	Ser	His	Met	Leu	Glu	Gln	Cys	Arg	His	Leu	Ser	
		515					520					525				
TAT	TCA	ATA	GGA	TTT	AAT	GGT	GAG	TTT	AAG	AAA	TTG	ACA	CCC	CTC	TAC	3429
Tyr	Ser	Ile	Gly	Phe	Asn	Gly	Glu	Phe	Lys	Lys	Leu	Thr	Pro	Leu	Tyr	
	530					535					540					
AAA	TTG	GAG	CAG	TTG	AGG	ACA	TTG	CTT	CCG	ATA	CGT	ATT	GAA	TTC	AGA	3477
Lys	Leu	Glu	Gln	Leu	Arg	Thr	Leu	Leu	Pro	Ile	Arg	Ile	Glu	Phe	Arg	
545					550					555					560	
TTG	CAC	AAT	CTA	AGC	AAG	AGG	GTG	TTG	CAT	AAC	ATA	CTG	CCT	ACA	CTA	3525
Leu	His	Asn	Leu	Ser	Lys	Arg	Val	Leu	His	Asn	Ile	Leu	Pro	Thr	Leu	
				565					570					575		
AGA	TCC	TTG	AGG	GCC	CTA	TCA	TTC	TCT	CAA	TAC	AAG	ATT	AAG	GAG	TTG	3573
Arg	Ser	Leu	Arg	Ala	Leu	Ser	Phe	Ser	Gln	Tyr	Lys	Ile	Lys	Glu	Leu	
			580					585					590			
CCA	AAT	GAC	TTG	TTT	ACC	AAA	TTA	AAG	CTC	CTC	AGA	TTT	TTG	GAT	ATT	3621
Pro	Asn	Asp	Leu	Phe	Thr	Lys	Leu	Lys	Leu	Leu	Arg	Phe	Leu	Asp	Ile	
		595					600					605				
TCT	CGG	ACA	TGG	ATT	ACA	AAG	TTG	CCG	GAT	TCC	ATT	TGT	GGA	TTA	TAT	3669
Ser	Arg	Thr	Trp	Ile	Thr	Lys	Leu	Pro	Asp	Ser	Ile	Cys	Gly	Leu	Tyr	
	610					615					620					
AAC	TTG	GAG	ACA	CTT	CTC	CTG	TCA	TCT	TGT	GCT	GAT	CTT	GAG	GAG	CTA	3717
Asn	Leu	Glu	Thr	Leu	Leu	Leu	Ser	Ser	Cys	Ala	Asp	Leu	Glu	Glu	Leu	
625					630					635					640	
CCG	CTG	CAG	ATG	GAG	AAG	TTG	ATT	AAC	TTG	CGT	CAT	CTT	GAC	GTA	AGC	3765
Pro	Leu	Gln	Met	Glu	Lys	Leu	Ile	Asn	Leu	Arg	His	Leu	Asp	Val	Ser	
				645					650					655		
AAC	ACT	CGG	CGC	TTG	AAG	ATG	CCA	CTA	CAT	CTG	AGC	AGG	TTG	AAA	AGC	3813
Asn	Thr	Arg	Arg	Leu	Lys	Met	Pro	Leu	His	Leu	Ser	Arg	Leu	Lys	Ser	
			660					665					670			
CTC	CAA	GTG	TTG	GTG	GGA	CCC	AAG	TTT	TTT	GTA	GAT	GGT	TGG	AGA	ATG	3861
Leu	Gln	Val	Leu	Val	Gly	Pro	Lys	Phe	Phe	Val	Asp	Gly	Trp	Arg	Met	
		675					680					685				
GAA	GAT	TTG	GGT	GAA	GCA	CAA	AAC	TTA	CAT	GGA	TCT	CTA	TCA	GTT	GTG	3909
Glu	Asp	Leu	Gly	Glu	Ala	Gln	Asn	Leu	His	Gly	Ser	Leu	Ser	Val	Val	
	690					695					700					
AAG	TTG	GAA	AAT	GTG	GTT	GAT	AGA	AGG	GAA	GCT	GTG	AAG	GCA	AAG	ATG	3957
Lys	Leu	Glu	Asn	Val	Val	Asp	Arg	Arg	Glu	Ala	Val	Lys	Ala	Lys	Met	
705					710					715					720	

AGG	GAG	AAG	AAT	CAT	GTT	GAG	CAA	TTA	TCA	TTG	GAG	TGG	AGT	GAA	AGT	4005
Arg	Glu	Lys	Asn	His	Val	Glu	Gln	Leu	Ser	Leu	Glu	Trp	Ser	Glu	Ser	
				725					730					735		
AGT	ATT	GCC	GAC	AAT	TCA	CAA	ACA	GAA	AGT	GAC	ATA	CTT	GAT	GAG	CTA	4053
Ser	Ile	Ala	Asp	Asn	Ser	Gln	Thr	Glu	Ser	Asp	Ile	Leu	Asp	Glu	Leu	
			740					745					750			
TGC	CCA	CAT	AAA	AAC	ATC	AAA	AAA	GTC	GAA	ATC	AGT	GGA	TAT	AGA	GGG	4101
Cys	Pro	His	Lys	Asn	Ile	Lys	Lys	Val	Glu	Ile	Ser	Gly	Tyr	Arg	Gly	
		755					760					765				
ACA	AAC	TTT	CCC	AAT	TGG	GTA	GCT	GAT	CCT	TTG	TTT	CTT	AAG	CTG	GTG	4149
Thr	Asn	Phe	Pro	Asn	Trp	Val	Ala	Asp	Pro	Leu	Phe	Leu	Lys	Leu	Val	
	770					775					780					
AAT	TTG	TCT	CTA	AGA	AAC	TGC	AAG	GAC	TGT	TAC	TCC	TTG	CCA	GCA	CTA	4197
Asn	Leu	Ser	Leu	Arg	Asn	Cys	Lys	Asp	Cys	Tyr	Ser	Leu	Pro	Ala	Leu	
785					790					795					800	
GGA	CAA	CTC	CCT	TGT	TTG	AAA	TTC	CTT	TCC	GTT	AAA	GGG	ATG	CAT	GGA	4245
Gly	Gln	Leu	Pro	Cys	Leu	Lys	Phe	Leu	Ser	Val	Lys	Gly	Met	His	Gly	
				805					810					815		
ATA	AGA	GTG	GTG	ACG	GAA	GAA	TTC	TAT	GGC	AGA	TTG	TCC	TCC	AAA	AAG	4293
Ile	Arg	Val	Val	Thr	Glu	Glu	Phe	Tyr	Gly	Arg	Leu	Ser	Ser	Lys	Lys	
			820					825					830			
CCT	TTT	AAC	TCT	CTA	GAG	AAG	CTT	GAA	TTT	GAA	GAT	ATG	ACG	GAG	TGG	4341
Pro	Phe	Asn	Ser	Leu	Glu	Lys	Leu	Glu	Phe	Glu	Asp	Met	Thr	Glu	Trp	
		835					840					845				
AAG	CAA	TGG	CAC	GCA	CTA	GGA	ATT	GGA	GAG	TTC	CCT	ACA	CTT	GAG	AAC	4389
Lys	Gln	Trp	His	Ala	Leu	Gly	Ile	Gly	Glu	Phe	Pro	Thr	Leu	Glu	Asn	
	850					855					860					
CTT	TCA	ATT	AAA	AAT	TGC	CCT	GAG	CTC	AGT	TTG	GAG	ATA	CCC	ATC	CAA	4437
Leu	Ser	Ile	Lys	Asn	Cys	Pro	Glu	Leu	Ser	Leu	Glu	Ile	Pro	Ile	Gln	
865					870					875					880	
TTT	TCA	AGT	TTA	AAA	AGG	TTA	GAA	GTT	AGT	GAT	TGT	CCA	GTT	GTT	TTT	4485
Phe	Ser	Ser	Leu	Lys	Arg	Leu	Glu	Val	Ser	Asp	Cys	Pro	Val	Val	Phe	
				885					890					895		
GAT	GAT	GCC	CAA	CTG	TTT	AGA	TCC	CAA	CTT	GAG	GCA	ATG	AAG	CAG	ATT	4533
Asp	Asp	Ala	Gln	Leu	Phe	Arg	Ser	Gln	Leu	Glu	Ala	Met	Lys	Gln	Ile	
			900					905				910				
GAG	GAA	ATA	GAT	ATA	TGT	GAT	TGT	AAC	TCT	GTT	ACC	TCC	TTT	CCT	TTT	4581
Glu	Glu	Ile	Asp	Ile	Cys	Asp	Cys	Asn	Ser	Val	Thr	Ser	Phe	Pro	Phe	
		915					920					925				
AGC	ATA	CTG	CCA	ACT	ACC	TTG	AAG	AGA	ATA	CAG	ATA	TCT	CGT	TGC	CCA	4629
Ser	Ile	Leu	Pro	Thr	Thr	Leu	Lys	Arg	Ile	Gln	Ile	Ser	Arg	Cys	Pro	
	930					935					940					
AAA	TTG	AAA	TTG	GAG	GCG	CCA	GTT	GGT	GAG	ATG	TTT	GTG	GAG	TAT	TTG	4677
Lys	Leu	Lys	Leu	Glu	Ala	Pro	Val	Gly	Glu	Met	Phe	Val	Glu	Tyr	Leu	
945					950					955					960	

AGA	GTG	AAT	GAT	TGT	GGT	TGT	GTA	GAT	GAT	ATA	TCA	CCT	GAG	TTT	CTC	4725
Arg	Val	Asn	Asp	Cys	Gly	Cys	Val	Asp	Asp	Ile	Ser	Pro	Glu	Phe	Leu	
				965					970					975		
CCA	ACA	GCA	CGT	CAA	TTG	AGT	ATT	GAA	AAT	TGC	CAG	AAC	GTT	ACT	AGG	4773
Pro	Thr	Ala	Arg	Gln	Leu	Ser	Ile	Glu	Asn	Cys	Gln	Asn	Val	Thr	Arg	
			980					985					990			
TTT	TTG	ATT	CCT	ACT	GCC	ACT	GAA	ACT	CTC	CGT	ATT	TCG	AAT	TGT	GAG	4821
Phe	Leu	Ile	Pro	Thr	Ala	Thr	Glu	Thr	Leu	Arg	Ile	Ser	Asn	Cys	Glu	
		995					1000					1005				
AAT	GTT	GAA	AAA	CTA	TCG	GTG	GCA	TGT	GGA	GGA	GCG	GCC	CAG	ATG	ACG	4869
Asn	Val	Glu	Lys	Leu	Ser	Val	Ala	Cys	Gly	Gly	Ala	Ala	Gln	Met	Thr	
	1010					1015					1020					
TCA	CTG	AAT	ATT	TGG	GGA	TGT	AAG	AAG	CTC	AAG	TGT	CTT	CCA	GAA	CTC	4917
Ser	Leu	Asn	Ile	Trp	Gly	Cys	Lys	Lys	Leu	Lys	Cys	Leu	Pro	Glu	Leu	
1025				1030					1035						1040	
CTT	CCA	TCT	CTC	AAG	GAA	CTG	CGT	CTG	TCT	GAT	TGT	CCA	GAA	ATA	GAA	4965
Leu	Pro	Ser	Leu	Lys	Glu	Leu	Arg	Leu	Ser	Asp	Cys	Pro	Glu	Ile	Glu	
				1045					1050					1055		
GGA	GAA	TTG	CCC	TTC	AAT	TTA	GAA	ATA	CTC	CGT	ATC	ATA	TAT	TGC	AAG	5013
Gly	Glu	Leu	Pro	Phe	Asn	Leu	Glu	Ile	Leu	Arg	Ile	Ile	Tyr	Cys	Lys	
			1060				1065						1070			
AAA	CTG	GTG	AAT	GGC	CGA	AAG	GAG	TGG	CAT	TTA	CAG	AGA	CTC	ACA	GAG	5061
Lys	Leu	Val	Asn	Gly	Arg	Lys	Glu	Trp	His	Leu	Gln	Arg	Leu	Thr	Glu	
		1075				1080						1085				
TTA	TGG	ATC	GAT	CAT	GAT	GGG	AGT	GAC	GAA	GAT	ATT	GAA	CAT	TGG	GAG	5109
Leu	Trp	Ile	Asp	His	Asp	Gly	Ser	Asp	Glu	Asp	Ile	Glu	His	Trp	Glu	
	1090					1095					1100					
TTG	CCT	TGT	TCT	ATT	CAG	AGA	CTT	ACC	ATA	AAG	AAT	CTT	AAA	ACA	TTA	5157
Leu	Pro	Cys	Ser	Ile	Gln	Arg	Leu	Thr	Ile	Lys	Asn	Leu	Lys	Thr	Leu	
1105					1110					1115					1120	
AGC	AGC	CAA	CAT	CTC	AAA	AGC	CTC	ACC	TCT	CTT	CAA	TAT	CTA	TGT	ATT	5205
Ser	Ser	Gln	His	Leu	Lys	Ser	Leu	Thr	Ser	Leu	Gln	Tyr	Leu	Cys	Ile	
				1125					1130					1135		
GAG	GGT	TAT	TTA	TCT	CAG	ATT	CAG	TCA	CAA	GGC	CAG	CTT	TCC	TCC	TTT	5253
Glu	Gly	Tyr	Leu	Ser	Gln	Ile	Gln	Ser	Gln	Gly	Gln	Leu	Ser	Ser	Phe	
			1140				1145						1150			
TCT	CAC	CTC	ACT	TCG	CTT	CAA	ACT	CTA	CAA	ATC	TGG	AAT	TTC	CTT	AAT	5301
Ser	His	Leu	Thr	Ser	Leu	Gln	Thr	Leu	Gln	Ile	Trp	Asn	Phe	Leu	Asn	
		1155				1160						1165				
CTC	CAA	TCA	CTT	GCT	GAA	TCA	GCA	CTG	CCC	TCC	TCC	CTC	TCT	CAC	CTG	5349
Leu	Gln	Ser	Leu	Ala	Glu	Ser	Ala	Leu	Pro	Ser	Ser	Leu	Ser	His	Leu	
	1170					1175					1180					
GAG	ATA	GAT	GAT	TGC	CCT	AAT	CTC	CAA	TCA	CTC	TTC	GAA	TCA	GCA	CTG	5397
Glu	Ile	Asp	Asp	Cys	Pro	Asn	Leu	Gln	Ser	Leu	Phe	Glu	Ser	Ala	Leu	
1185				1190						1195					1200	

CCC TCC TCC CTC TCT CAG CTG TTC ATC CAG GAT TGC CCT AAT CTC CAA	5445
Pro Ser Ser Leu Ser Gln Leu Phe Ile Gln Asp Cys Pro Asn Leu Gln	
1205 1210 1215	
TCC CTT CCA TTT AAA GGG ATG CCC TCT TCC CTC TCT AAA CTA TCT ATT	5493
Ser Leu Pro Phe Lys Gly Met Pro Ser Ser Leu Ser Lys Leu Ser Ile	
1220 1225 1230	
TTC AAT TGC CCA TTG CTC ACA CCA CTA CTA GAA TTT GAC AAG GGG GAA	5541
Phe Asn Cys Pro Leu Leu Thr Pro Leu Leu Glu Phe Asp Lys Gly Glu	
1235 1240 1245	
TAC TGG CCA CAA ATT GCT CAT ATT CCC ATC ATA AAT ATC GAT TGG AAA	5589
Tyr Trp Pro Gln Ile Ala His Ile Pro Ile Ile Asn Ile Asp Trp Lys	
1250 1255 1260	
TAT ATT TAACAATTAA AACAAATGGC TCTCCAACCTG ATGTAAGCTA TTCGTTACCC	5645
Tyr Ile	
1265	
TTAGAAGCTT TTTATGATTC TATGTTTCTC ATTGCTTATT GGTTTATGCT CTTACCGTGT	5705
TTTAATTCAC GTCTCAATTG CCACCATGTT TAATCGAAAG TTTT TAGTTC TTGTAATCAT	5765
CAACCATCCT ATGTCACCTAG AAATTTTGAT AGGTAAAAGA GGTAGACAAA AAAGCTAAAC	5825
ATCTTTTTTC TTTCGTATAG CGACCAAACA ACTACATTTT GATAGGTAAG GGCTATAGAT	5885
ATACATTTGC AGGGTGTTAA ACCAAGGAGT AAGAAAATCA CTGTCTTCAG ATATCTTCTC	5945
TTGCATATAC TTTTGCAATT TTAAGCTACA TTTTGAAGTC ATGTGTTGTT GCTAACTTAA	6005
ACATGTTTTG TGCTTAATCA GATGTGGATT TTGAAGAGCG AGTACGACAA GTCTGGTACA	6065
TTAATTGTCC GTAGAAGTGT TTCTAAGGTG CTGCTGCTAT TTTTACATCT GTTCCCGAGT	6125
TTTGTTTTTT TTTTAAATCT TTCCACTAAA GCTATTATGT CGTCCACAGT GAATTTTCAG	6185
GTCTGTTGTT ATAGGCAAGT CTTTGAGATG CGACTATCAA AGAAGGGCGA TTACAATCAG	6245
TGTACCGCTG AAACATTTTC ATGTTTCCAG TGCAAGCCTC TTTTGTAAGT TGACAAACTC	6305
GATTAGTTAA TATGTTTGGG ACTCAACTAG TGGTTAGAGT ACTCATTTTG TAAGACTTGT	6365
GTACAGAAAA TCAAATTAGA ATTATAACTC GTGATGGTTG AATAAACTCT AAGAAGTACT	6425
GATATATTTT TTAGTGGATA TGTTGTTTGC TCATTCGGTG TTTGATATCC ACATTGGAGT	6485
CCAACTAAAT TCGAATTTGC ACAATCGAAG GAGCGGTGCT CCTGGCATGA TTTTTTTCCC	6545
ATTCTACGAC TAGTGCTCCT AAATTCTAAT TAAGCATAGA AAAATCTCAA CTATCTCACC	6605
CAACTCATAT CAGGATAGAG TATTCCTGA GGAGGATTCC TTCAGTTACA AAA	6658

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1266 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Glu	Ile	Gly	Leu	Ala	Val	Gly	Gly	Ala	Phe	Leu	Ser	Ser	Ala	Leu	1	5	10	15
Asn	Val	Leu	Phe	Asp	Arg	Leu	Ala	Pro	Asn	Gly	Asp	Leu	Leu	Asn	Met	20	25	30	
Phe	Arg	Lys	His	Lys	Asp	His	Val	Lys	Leu	Leu	Lys	Lys	Leu	Lys	Met	35	40	45	
Thr	Leu	Arg	Gly	Ile	Gln	Ile	Val	Leu	Ser	Asp	Ala	Glu	Asn	Lys	Gln	50	55	60	
Ala	Ser	Asn	Pro	Ser	Val	Arg	Asp	Trp	Leu	Asn	Glu	Leu	Arg	Asp	Ala	65	70	75	80
Val	Asp	Ser	Ala	Glu	Asn	Leu	Ile	Glu	Glu	Val	Asn	Tyr	Glu	Ala	Leu	85	90	95	
Arg	Leu	Lys	Val	Glu	Gly	Gln	His	Gln	Asn	Phe	Ser	Glu	Thr	Ser	Asn	100	105	110	
Gln	Gln	Val	Ser	Asp	Asp	Phe	Phe	Leu	Asn	Ile	Lys	Asp	Lys	Leu	Glu	115	120	125	
Asp	Thr	Ile	Glu	Thr	Leu	Lys	Asp	Leu	Gln	Glu	Gln	Ile	Gly	Leu	Leu	130	135	140	
Gly	Leu	Lys	Glu	Tyr	Phe	Asp	Ser	Thr	Lys	Leu	Glu	Thr	Arg	Arg	Pro	145	150	155	160
Ser	Thr	Ser	Val	Asp	Asp	Glu	Ser	Asp	Ile	Phe	Gly	Arg	Gln	Ser	Glu	165	170	175	
Ile	Glu	Asp	Leu	Ile	Asp	Arg	Leu	Leu	Ser	Glu	Gly	Ala	Ser	Gly	Lys	180	185	190	
Lys	Leu	Thr	Val	Val	Pro	Ile	Val	Gly	Met	Gly	Gly	Gln	Gly	Lys	Thr	195	200	205	
Thr	Leu	Ala	Lys	Ala	Val	Tyr	Asn	Asp	Glu	Arg	Val	Lys	Asn	His	Phe	210	215	220	
Asp	Leu	Lys	Ala	Trp	Tyr	Cys	Val	Ser	Glu	Gly	Phe	Asp	Ala	Leu	Arg	225	230	235	240
Ile	Thr	Lys	Glu	Leu	Leu	Gln	Glu	Ile	Gly	Lys	Phe	Asp	Ser	Lys	Asp	245	250	255	
Val	His	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Val	Lys	Leu	Lys	Glu	Ser	Leu	260	265	270	
Lys	Gly	Lys	Lys	Phe	Leu	Ile	Val	Leu	Asp	Asp	Val	Trp	Asn	Glu	Asn	275	280	285	
Tyr	Asn	Glu	Trp	Asn	Asp	Leu	Arg	Asn	Ile	Phe	Ala	Gln	Gly	Asp	Ile	290	295	300	

Gly	Ser	Lys	Ile	Ile	Val	Thr	Thr	Arg	Lys	Asp	Ser	Val	Ala	Leu	Met	305	310	315	320
Met	Gly	Asn	Glu	Gln	Ile	Arg	Met	Gly	Asn	Leu	Ser	Thr	Glu	Ala	Ser		325	330	335
Trp	Ser	Leu	Phe	Gln	Arg	His	Ala	Phe	Glu	Asn	Met	Asp	Pro	Met	Gly		340	345	350
His	Pro	Glu	Leu	Glu	Glu	Val	Gly	Arg	Gln	Ile	Ala	Ala	Lys	Cys	Lys		355	360	365
Gly	Leu	Pro	Leu	Ala	Leu	Lys	Thr	Leu	Ala	Gly	Met	Leu	Arg	Ser	Lys		370	375	380
Ser	Glu	Val	Glu	Glu	Trp	Lys	Arg	Ile	Leu	Arg	Ser	Glu	Ile	Trp	Glu		385	390	395
Leu	Pro	His	Asn	Asp	Ile	Leu	Pro	Ala	Leu	Met	Leu	Ser	Tyr	Asn	Asp		405	410	415
Leu	Pro	Ala	His	Leu	Lys	Arg	Cys	Phe	Ser	Phe	Cys	Ala	Ile	Phe	Pro		420	425	430
Lys	Asp	Tyr	Pro	Phe	Arg	Lys	Glu	Gln	Val	Ile	His	Leu	Trp	Ile	Ala		435	440	445
Asn	Gly	Leu	Val	Pro	Val	Lys	Asp	Glu	Ile	Asn	Gln	Asp	Leu	Gly	Asn		450	455	460
Gln	Tyr	Phe	Leu	Glu	Leu	Arg	Ser	Arg	Ser	Leu	Phe	Glu	Lys	Val	Pro		465	470	475
Asn	Pro	Ser	Lys	Arg	Asn	Ile	Glu	Glu	Leu	Phe	Leu	Met	His	Asp	Leu		485	490	495
Val	Asn	Asp	Leu	Ala	Gln	Leu	Ala	Ser	Ser	Lys	Leu	Cys	Ile	Arg	Leu		500	505	510
Glu	Glu	Ser	Gln	Gly	Ser	His	Met	Leu	Glu	Gln	Cys	Arg	His	Leu	Ser		515	520	525
Tyr	Ser	Ile	Gly	Phe	Asn	Gly	Glu	Phe	Lys	Lys	Leu	Thr	Pro	Leu	Tyr		530	535	540
Lys	Leu	Glu	Gln	Leu	Arg	Thr	Leu	Leu	Pro	Ile	Arg	Ile	Glu	Phe	Arg		545	550	555
Leu	His	Asn	Leu	Ser	Lys	Arg	Val	Leu	His	Asn	Ile	Leu	Pro	Thr	Leu		565	570	575
Arg	Ser	Leu	Arg	Ala	Leu	Ser	Phe	Ser	Gln	Tyr	Lys	Ile	Lys	Glu	Leu		580	585	590
Pro	Asn	Asp	Leu	Phe	Thr	Lys	Leu	Lys	Leu	Leu	Arg	Phe	Leu	Asp	Ile		595	600	605
Ser	Arg	Thr	Trp	Ile	Thr	Lys	Leu	Pro	Asp	Ser	Ile	Cys	Gly	Leu	Tyr		610	615	620

Asn 625	Leu	Glu	Thr	Leu	Leu 630	Leu	Ser	Ser	Cys	Ala 635	Asp	Leu	Glu	Glu	Leu 640
Pro	Leu	Gln	Met	Glu 645	Lys	Leu	Ile	Asn	Leu 650	Arg	His	Leu	Asp	Val 655	Ser
Asn	Thr	Arg	Arg 660	Leu	Lys	Met	Pro	Leu 665	His	Leu	Ser	Arg	Leu 670	Lys	Ser
Leu	Gln	Val 675	Leu	Val	Gly	Pro	Lys 680	Phe	Phe	Val	Asp	Gly 685	Trp	Arg	Met
Glu 690	Asp	Leu	Gly	Glu	Ala	Gln 695	Asn	Leu	His	Gly	Ser 700	Leu	Ser	Val	Val
Lys 705	Leu	Glu	Asn	Val 710	Val	Asp	Arg	Arg	Glu	Ala 715	Val	Lys	Ala	Lys	Met 720
Arg	Glu	Lys	Asn 725	His	Val	Glu	Gln	Leu 730	Ser	Leu	Glu	Trp	Ser	Glu 735	Ser
Ser	Ile	Ala	Asp 740	Asn	Ser	Gln	Thr	Glu 745	Ser	Asp	Ile	Leu	Asp 750	Glu	Leu
Cys	Pro	His 755	Lys	Asn	Ile	Lys	Lys 760	Val	Glu	Ile	Ser	Gly 765	Tyr	Arg	Gly
Thr 770	Asn	Phe	Pro	Asn	Trp	Val 775	Ala	Asp	Pro	Leu	Phe 780	Leu	Lys	Leu	Val
Asn 785	Leu	Ser	Leu	Arg	Asn 790	Cys	Lys	Asp	Cys	Tyr 795	Ser	Leu	Pro	Ala	Leu 800
Gly	Gln	Leu	Pro	Cys 805	Leu	Lys	Phe	Leu 810	Ser	Val	Lys	Gly	Met	His 815	Gly
Ile	Arg	Val 820	Val	Thr	Glu	Glu	Phe	Tyr 825	Gly	Arg	Leu	Ser	Ser 830	Lys	Lys
Pro	Phe	Asn 835	Ser	Leu	Glu	Lys	Leu 840	Glu	Phe	Glu	Asp	Met 845	Thr	Glu	Trp
Lys 850	Gln	Trp	His	Ala	Leu	Gly 855	Ile	Gly	Glu	Phe	Pro 860	Thr	Leu	Glu	Asn
Leu 865	Ser	Ile	Lys	Asn	Cys 870	Pro	Glu	Leu	Ser	Leu 875	Glu	Ile	Pro	Ile	Gln 880
Phe	Ser	Ser	Leu	Lys 885	Arg	Leu	Glu	Val 890	Ser	Asp	Cys	Pro	Val	Val 895	Phe
Asp	Asp	Ala	Gln 900	Leu	Phe	Arg	Ser	Gln 905	Leu	Glu	Ala	Met	Lys 910	Gln	Ile
Glu	Glu	Ile 915	Asp	Ile	Cys	Asp	Cys 920	Asn	Ser	Val	Thr	Ser 925	Phe	Pro	Phe
Ser 930	Ile	Leu	Pro	Thr	Thr 935	Leu	Lys	Arg	Ile	Gln	Ile 940	Ser	Arg	Cys	Pro

Lys	Leu	Lys	Leu	Glu	Ala	Pro	Val	Gly	Glu	Met	Phe	Val	Glu	Tyr	Leu	945	950	955				960
Arg	Val	Asn	Asp	Cys	Gly	Cys	Val	Asp	Asp	Ile	Ser	Pro	Glu	Phe	Leu		965	970				975
Pro	Thr	Ala	Arg	Gln	Leu	Ser	Ile	Glu	Asn	Cys	Gln	Asn	Val	Thr	Arg		980	985				990
Phe	Leu	Ile	Pro	Thr	Ala	Thr	Glu	Thr	Leu	Arg	Ile	Ser	Asn	Cys	Glu		995	1000			1005	
Asn	Val	Glu	Lys	Leu	Ser	Val	Ala	Cys	Gly	Gly	Ala	Ala	Gln	Met	Thr	1010		1015			1020	
Ser	Leu	Asn	Ile	Trp	Gly	Cys	Lys	Lys	Leu	Lys	Cys	Leu	Pro	Glu	Leu	1025		1030			1035	1040
Leu	Pro	Ser	Leu	Lys	Glu	Leu	Arg	Leu	Ser	Asp	Cys	Pro	Glu	Ile	Glu		1045	1050				1055
Gly	Glu	Leu	Pro	Phe	Asn	Leu	Glu	Ile	Leu	Arg	Ile	Ile	Tyr	Cys	Lys		1060	1065			1070	
Lys	Leu	Val	Asn	Gly	Arg	Lys	Glu	Trp	His	Leu	Gln	Arg	Leu	Thr	Glu		1075	1080			1085	
Leu	Trp	Ile	Asp	His	Asp	Gly	Ser	Asp	Glu	Asp	Ile	Glu	His	Trp	Glu	1090		1095			1100	
Leu	Pro	Cys	Ser	Ile	Gln	Arg	Leu	Thr	Ile	Lys	Asn	Leu	Lys	Thr	Leu	1105		1110			1115	1120
Ser	Ser	Gln	His	Leu	Lys	Ser	Leu	Thr	Ser	Leu	Gln	Tyr	Leu	Cys	Ile		1125	1130				1135
Glu	Gly	Tyr	Leu	Ser	Gln	Ile	Gln	Ser	Gln	Gly	Gln	Leu	Ser	Ser	Phe		1140	1145				1150
Ser	His	Leu	Thr	Ser	Leu	Gln	Thr	Leu	Gln	Ile	Trp	Asn	Phe	Leu	Asn		1155	1160			1165	
Leu	Gln	Ser	Leu	Ala	Glu	Ser	Ala	Leu	Pro	Ser	Ser	Leu	Ser	His	Leu	1170		1175			1180	
Glu	Ile	Asp	Asp	Cys	Pro	Asn	Leu	Gln	Ser	Leu	Phe	Glu	Ser	Ala	Leu	1185		1190			1195	1200
Pro	Ser	Ser	Leu	Ser	Gln	Leu	Phe	Ile	Gln	Asp	Cys	Pro	Asn	Leu	Gln		1205	1210				1215
Ser	Leu	Pro	Phe	Lys	Gly	Met	Pro	Ser	Ser	Leu	Ser	Lys	Leu	Ser	Ile		1220	1225				1230
Phe	Asn	Cys	Pro	Leu	Leu	Thr	Pro	Leu	Leu	Glu	Phe	Asp	Lys	Gly	Glu	1235		1240			1245	

Tyr Trp Pro Gln Ile Ala His Ile Pro Ile Ile Asn Ile Asp Trp Lys
1250 1255 1260

Tyr Ile
1265